RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/653,681B_

Source: _1Fw16_

Date Processed by STIC: _7/14/05_

ENTERED

Serial Number: 10/653,681B   CRF Edit Date: 7/15/05
                                   Edited by: ___

_____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

_____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

✓ Inserted or (corrected) a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

5

_____

_____ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

_____ Inserted mandatory headings/numeric identifiers, specifically:

_____

_____ Moved responses to same line as heading/numeric identifier, specifically:

_____

✓ Other: Sequence 5- reduced blank spaces between groups of 10 bases

_____

Revised 09/09/2003

IFW16

RAW SEQUENCE LISTING   DATE: 07/15/2005
PATENT APPLICATION: US/10/653,681B   TIME: 12:24:17

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\07152005\J653681B.raw**

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 3  <110> APPLICANT: DAI, KEN-SHWO
 5  <120> TITLE OF INVENTION: HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER
 7  <130> FILE REFERENCE: U014798-3
 9  <140> CURRENT APPLICATION NUMBER: 10/653,681B
10  <141> CURRENT FILING DATE: 2003-09-02
12  <160> NUMBER OF SEQ ID NOS: 6
14  <170> SOFTWARE: PatentIn version 3.2
16  <210> SEQ ID NO: 1
17  <211> LENGTH: 1090
18  <212> TYPE: DNA
19  <213> ORGANISM: ARTIFICIAL SEQUENCE
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22  <223> OTHER INFORMATION: VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE
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26  <221> NAME/KEY: CDS
27  <222> LOCATION: (70)..(333)
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34             1               5                  10
36  att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa     159
37  Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu
38  15                  20                  25                  30
40  gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc     207
41  Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala
42                      35                  40                  45
44  tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag     255
45  Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys
46                  50                  55                  60
48  atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag     303
49  Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys
50              65                  70                  75
52  ttg tgg ccc act tcc aga tcg aga agc tct tgaacaaacc tggactgaaa       353
53  Leu Trp Pro Thr Ser Arg Ser Arg Ser Ser
54      80                  85
56  tataaaccag tgactaacca ggttgagtgt cacccatacc tcacgcagga gaaactgatc    413
58  cagtactgcc actccaaggg catcaccgtt acggcctaca gcccctgggg ctctccggat    473
60  agaccttggg ccaagccaga agacccttcc ctgctggagg atcccaagat taaggagatt    533
62  gctgcaaagc acaaaaaaac cgcagcccag gttctgatcc gtttccatat ccagaggaat    593
64  gtgattgtca tccccaagtc tgtgacacca gcacgcattg ttgagaacat tcaggtcttt    653
66  gactttaaat tgagtgatga ggagatggca accatactca gcttcaacag aaactggagg    713
68  gcctgtaacg tgttgcaatc ctctcatttg gaagactatc ccttcgatgc agaatattga    773
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RAW SEQUENCE LISTING   DATE: 07/15/2005
PATENT APPLICATION: US/10/653,681B   TIME: 12:24:17

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\07152005\J653681B.raw**

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 70 ggttgaatct cctggtgaga ttatacagga gattctcttt cttcgctgaa gtgtgactac    833
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 74 atagacgaga atcgaggtgc tgtttttagac atttatttct gtatgttcaa ctaggatcag   953
 76 aatatcacag aaaagcatgg cttgaataag gaaatgacaa ttttttccac ttatctgatc   1013
 78 agaacaaatg tttattaagc atcagaaact ctgccaacac tgaggatgta aagatcaata   1073
 80 aaaaaaataa taatcat                                                   1090
 83 <210> SEQ ID NO: 2
 84 <211> LENGTH: 88
 85 <212> TYPE: PRT
 86 <213> ORGANISM: ARTIFICIAL SEQUENCE
 88 <220> FEATURE:
 89 <223> OTHER INFORMATION: PEPTIDE ENCODED BY VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE
GENE
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 94 1               5                   10                  15
 97 Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
 98             20                  25                  30
101 Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
102         35                  40                  45
105 Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
106     50                  55                  60
109 Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp
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127 <221> NAME/KEY: CDS
128 <222> LOCATION: (70)..(804)
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134           Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro
135            1               5                   10
137 att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa     159
138 Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu
139 15                  20                  25                  30
141 gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc     207
142 Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala
143             35                  40                  45
145 tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag     255
146 Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys
147         50                  55                  60
149 atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag     303
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153 ttg tgg ccc act ttc ttt gag aga ccc ctt gtg agg aaa gcc ttt gag      351
154 Leu Trp Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu
155         80                  85                  90
157 aag acc ctc aag gac ctg aag ctg agc tat ctg gac gtc tat ctt att      399
158 Lys Thr Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile
159 95                  100                 105                 110
161 cac tgg cca cag gga ttc aag tct ggg gat gac ctt ttc ccc aaa gat      447
162 His Trp Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp
163                 115                 120                 125
165 gat aaa ggt aat gcc atc ggt gga aaa gca acg ttc ttg gat gcc tgg      495
166 Asp Lys Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp
167                 130                 135                 140
169 gag gcc atg gag gag ctg gtg gat gag ggg ctg gtg aaa gcc ctt ggg      543
170 Glu Ala Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly
171         145                 150                 155
173 gtc tcc aat ttc agc cac ttc cag atc gag aag ctc ttg aac aaa cct      591
174 Val Ser Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro
175         160                 165                 170
177 gga ctg aaa tat aaa cca gtg act aac cag gtt gag tgt cac cca tac      639
178 Gly Leu Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr
179 175                 180                 185                 190
181 ctc acg cag gag aaa ctg atc cag tac tgc cac tcc aag ggc atc acc      687
182 Leu Thr Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr
183                 195                 200                 205
185 gtt acg gcc tac agc ccc ctg ggc tct ccg gat aga cct tgg gcc aag      735
186 Val Thr Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys
187                 210                 215                 220
189 cca gaa gac cct tcc ctg ctg gag gat ccc aag att aag gag att gct      783
190 Pro Glu Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala
191         225                 230                 235
193 gca aag cac tcc cca agt ctg tgacaccagc acgcattgtt gagaacattc        834
194 Ala Lys His Ser Pro Ser Leu
195         240                 245
197 aggtctttga ctttaaattg agtgatgagg agatggcaac catactcagc ttcaacagaa    894
199 actggagggc ctgtaacgtg ttgcaatcct ctcatttgga agactatccc ttcgatgcag    954
201 aatattgagg ttgaatctcc tggtgagatt atacaggaga ttctctttct tcgctgaagt   1014
203 gtgactacct ccactcatgt cccatttttag ccaagcttat ttaagatcac agtgaactta  1074
205 gtcctgttat agacgagaat cgaggtgctg ttttagacat ttatttctgt atgttcaact   1134
207 aggatcagaa tatcacagaa aagcatggct tgaataagga aatgacaatt ttttccactt   1194
209 atctgatcag aacaaatgtt tattaagcat cagaaactct gccaacactg aggatgtaaa   1254
211 gatcaataaa aaaaataata atcat                                         1279
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215 <211> LENGTH: 245
216 <212> TYPE: PRT
217 <213> ORGANISM: ARTIFICIAL SEQUENCE
219 <220> FEATURE:
220 <223> OTHER INFORMATION: PEPTIDE ENCODED BY VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE
GENE
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229             20                  25              30
232 Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
233         35                  40                  45
236 Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
237     50                  55                  60
240 Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp
241 65                  70                  75                  80
244 Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu Lys Thr
245                 85                  90                  95
248 Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile His Trp
249             100                 105                 110
252 Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp Asp Lys
253         115                 120                 125
256 Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp Glu Ala
257     130                 135                 140
260 Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly Val Ser
261 145                 150                 155                 160
264 Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro Gly Leu
265             165                 170                 175
268 Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr Leu Thr
269             180                 185                 190
272 Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr Val Thr
273         195                 200                 205
276 Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys Pro Glu
277     210                 215                 220
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281 225                 230                 235                 240
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285             245
287 <210> SEQ ID NO: 5
289 <211> LENGTH: 1337
291 <212> TYPE: DNA
293 <213> ORGANISM: HOMO SAPIEN
295 <220> FEATURE:
297 <223> OTHER INFORMATION: HUMAN ARL GENE
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303 ctgggcactt ggaagtctcc tctcggcaaa gtgaaagaag cagtgaaggt ggccattgat   180
304 gcaggatatc ggcacattga ctgtgcctat gtctatcaga atgaacatga agtggggga   240
305 gccatccaag agaagatcca agagaaggct gtgaagcggg aggacctgtt catcgtcagc   300
306 aagttgtggc ccactttctt tgagagaccc cttgtgagga aagcctttga gaagaccctc   360
307 aaggacctga gctgagcta tctggacgtc tatcttattc actggccaca gggattcaag   420
308 tctggggatg acctttt ccc caaagatgat aaaggtaatg ccatcggtgg aaaagcaacg   480
309 ttcttggatg cctgggaggc catggaggag ctggtggatg aggggctggt gaaagccctt   540
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312 cagtactgcc actccaaggg catcaccgtt acggcctaca gccccctggg ctctccggat     720
313 agaccttggg ccaagccaga agacccttcc ctgctggagg atcccaagat taaggagatt     780
314 gctgcaaagc acaaaaaaac cgcagcccag gttctgatcc gtttccatat ccagaggaat     840
315 gtgattgtca tccccaagtc tgtgacacca gcacgcattg ttgagaacat tcaggtcttt     900
316 gactttaaat tgagtgatga ggagatggca accatactca gcttcaacag aaactggagg     960
317 gcctgtaacg tgttgcaatc ctctcatttg gaagactatc ccttcgatgc agaatattga    1020
318 ggttgaatct cctggtgaga ttatacagga gattctcttt cttcgctgaa gtgtgactac    1080
319 ctccactcat gtcccatttt agccaagctt atttaagatc acagtgaact tagtcctgtt    1140
320 atagacgaga atcgaggtgc tgttttagac atttatttct gtatgttcaa ctaggatcag    1200
321 aatatcacag aaaagcatgg cttgaataag gaaatgacaa ttttttccac ttatctgatc    1260
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327 <211> LENGTH: 316
329 <212> TYPE: PRT
331 <213> ORGANISM: HOMO SAPIEN
333 <220> FEATURE:
335 <223> OTHER INFORMATION: AMINO ACID SEQUENCE ENCODED BY HUMAN ARL GENE
337 <400> SEQUENCE: 6
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343                  20                  25                  30
345 Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
346              35                  40                  45
348 Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
349      50                  55                  60
351 Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp
352 65                  70                  75                  80
354 Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu Lys Thr
355                  85                  90                  95
357 Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile His Trp
358                 100                 105                 110
360 Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp Asp Lys
361             115                 120                 125
363 Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp Glu Ala
364     130                 135                 140
366 Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly Val Ser
367 145                 150                 155                 160
369 Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro Gly Leu
370                 165                 170                 175
372 Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr Leu Thr
373             180                 185                 190
375 Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr Val Thr
376             195                 200                 205
378 Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys Pro Glu
379     210                 215                 220
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VERIFICATION SUMMARY   DATE: 07/15/2005
PATENT APPLICATION: **US/10/653,681B**   TIME: 12:24:19

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\07152005\J653681B.raw**

Raw Sequence Listing before editing,
for reference only

IFW16

RAW SEQUENCE LISTING   DATE: 07/14/2005
PATENT APPLICATION: US/10/653,681B   TIME: 12:29:14

Input Set : A:\U0147983 SEQUENCE LISTING.txt
Output Set: N:\CRF4\07142005\J653681B.raw

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  3 <110> APPLICANT: DAI, KEN-SHWO
  5 <120> TITLE OF INVENTION: HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER
  7 <130> FILE REFERENCE: U014798-3
  9 <140> CURRENT APPLICATION NUMBER: 10/653,681B
 10 <141> CURRENT FILING DATE: 2003-09-02
 12 <160> NUMBER OF SEQ ID NOS: 6
 14 <170> SOFTWARE: PatentIn version 3.2
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Does Not Comply — Corrected Diskette Needed

ERRORED SEQUENCES

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287 <210> SEQ ID NO: 5
289 <211> LENGTH: 1337
291 <212> TYPE: DNA
293 <213> ORGANISM: HOMO SAPIEN
295 <220> FEATURE:
297 <223> OTHER INFORMATION: HUMAN ARL GENE
299 <400> SEQUENCE: 5
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(handwritten: delete extra spaces — per Sequence Rules, only one space between groups of 10)

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306 gccatccaag  agaagatcca  agagaaggct  gtgaagcggg  aggacctgtt  catcgtcagc  300
307 aagttgtggc  ccactttctt  tgagagaccc  cttgtgagga  aagcctttga  gaagaccctc  360
308 aaggacctga  agctgagcta  tctggacgtc  tatcttattc  actggccaca  gggattcaag  420
309 tctggggatg  accttttccc  caaagatgat  aaaggtaatg  ccatcggtgg  aaaagcaacg  480
310 ttcttggatg  cctgggaggc  catggaggag  ctggtggatg  aggggctggt  gaaagccctt  540
311 ggggtctcca  atttcagcca  cttccagatc  gagaagctct  tgaacaaacc  tggactgaaa  600
312 tataaaccag  tgactaacca  ggttgagtgt  cacccatacc  tcacgcagga  gaaactgatc  660
313 cagtactgcc  actccaaggg  catcaccgtt  acggcctaca  gcccccctggg ctctccggat  720
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E--> 323
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same error

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                                            aaaaaaataa    taatcat
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aagatcaata   1320

taatcat

1380 1337   aaaaaaataa

Input Set : A:\U0147983 SEQUENCE LISTING.txt
Output Set: N:\CRF4\07142005\J653681B.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:5; Line(s) 301,302,303,304,305,306,307,308,309,310,311,312,313,314,315
Seq#:5; Line(s) 316,317,318,319,320,321,322,323

VERIFICATION SUMMARY   DATE: 07/14/2005
PATENT APPLICATION: US/10/653,681B   TIME: 12:29:15

Input Set : **A:\U0147983 SEQUENCE LISTING.txt**
Output Set: **N:\CRF4\07142005\J653681B.raw**

L:323 M:254 E: No. of Bases conflict, LENGTH:Input:1380 Counted:1337 SEQ:5